

Figure 1(A)

<u>GGATCGTCTCAGGTCAGCGGAGGGA</u>	25
SL33	
<u>GGAGACTTATAGACCTATCCAGTCT</u>	50
TCAAGGTGCTCCAGAAAGCAGGAGT	75
TGAAGACCTGGGTGTGAGGGACACA	100
TACATCCTAAAAGCACCACAGCAGA	125
GGAGGCCCCAGGCAGTGCCAGGAGTC	150
AAGGTTCCCAGAAGACAAACCCCCT	175
AGGAAGACAGGCGACCTGTGAGGCC	200
<u>CTAGAGCACCACTTAAGAGAAGAA</u>	225
SL34	
GAGCTGTAAGCCGGCCTTTGTCAGA	250
GCCATCATGGGGGACAAGGATATGC	275
CTACTGCTGGGATGCCGAGTCTTCT	300
CCAGAGTTCCTCTGAGAGTCCTCAG	325
AGTTGTCCTGAGGGGGAGGACTCCC	350
AGTCTCCTCTCCAGATTCCCCAGAG	375
TTCTCCTGAGAGCGACGACACCCTG	400
TATCCTCTCCAGAGTCCTCAGAGTC	425
GTTCTGAGGGGGAGGACTCCTCGGA	450
TCCTCTCCAGAGACCTCCTGAGGGG	475
AAGGACTCCCAGTCTCCTCTCCAGA	500
TTCCCCAGAGTTCTCCTGAGGGCGA	525
CGACACCCAGTCTCCTCTCCAGAAT	550
TCTCAGAGTTCTCCTGAGGGGAAGG	575
ACTCCCTGTCTCCTCTAGAGATTTT	600
TCAGAGCCCTCCTGAGGGTGAGGAT	625
GTCCAGTCTCCTCTGCAGAATCCTG	650
CGAGTTCCTTCTTCTCCTCTGCTTT	675
ATTGAGTATTTTCCAGAGTTCCCCT	700

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Figure 1(B)

GAGAGAACTCAGAGTACTTTTGAGG 725
GTTTTCCCCAGTCTCCTCTCCAGAT 750
TCCTGTGAGCTCCTCCTCCTCCTCC 775
ACTTTATTGAGTCTTTTCCAGAGTT 800
CCCCTGAGAGAACTCAGAGTACTTT 825
TGAGGGTTTTCCCCAGTCTCTTCTC 850
CAGATTCCTATGACCTCCTCCTTCT 875
CCTCTACTTTATTGAGTATTTTCCA 900
GAGTTCTCCTGAGAGTGCTCAAAGT 925
ACTTTTGAGGGTTTTCCCCAGTCTC 950
CTCTCCAGATTCCTGGGAGCCCCCTC 975
CTTCTCCTCCACTTTACTGAGTCTT 1000
TTCCAGAGTTCCCCTGAGAGAACTC 1025
ACAGTACTTTTGAGGGTTTTCCCCA 1050
GTCTCCTCTCCAGATTCCTATGACC 1075
TCCTCCTTCTCCTCTACTTTATTGA 1100
GTATTTTCCAGAGTTCTCCTGAGAG 1125
TGCTCAAAGTACTTTTGAGGGTTTT 1150
CCCCAGTCTCCTCTCCAGATTCCTG 1175
GGAGCCCCTCCTTCTCCTCCACTTT 1200
ACTGAGTCTTTTCCAGAGTCCCCT 1225
GAGAGAACTCACAGTACTTTTGAGG 1250
GTTTTCCCCAGTCTCCTCTCCAGAT 1275
TCCTATGACCTCCTCCTTCTCCTCT 1300
ACTTTATTGAGTATTTTACAGAGTT 1325
CTCCTGAGAGTGCTCAAAGTGCTTT 1350
TGAGGGTTTTCCCCAGTCTCCTCTC 1375
CAGATTCCTGTGAGCTCCTCTTTCT 1400

Figure 1(C)

CCTACACTTTATTGAGTCTTTTCCA 1425
GAGTTCCCCTGAGAGAACTCAGAGT 1450
ACTTTTGAGGGTTTCCCCAGTCTC 1475
CTCTCCAGATTCCTGTGAGCTCCTC 1500
CTCCTCCTCCTCCACTTTATTGAGT 1525
CTTTTCCAGAGTTCCCCTGAGTGTA 1550
CTCAAAGTACTTTTGAGGGTTTCC 1575
CCAGTCTCCTCTCCAGATTCCTCAG 1600
AGTCCTCCTGAAGGGGAGAATACCC 1625
ATTCTCCTCTCCAGATTGTTCCAAG 1650
TCTTCCTGAGTGGGAGGACTCCCTG 1675
TCTCCTCACTACTTTCCTCAGAGCC 1700
CTCCTCAGGGGGAGGACTCCCTATC 1725
TCCTCACTACTTTCCTCAGAGCCCT 1750
CCTCAGGGGGAGGACTCCCTGTCTC 1775
CTCACTACTTTCCTCAGAGCCCTCA 1800
GGGGGAGGACTCCCTGTCTCCTCAC 1825
TACTTTCCTCAGAGCCCTCCTCAGG 1850
GGGAGGACTCCATGTCTCCTCTCTA 1875
CTTTCCTCAGAGTCCTCTTCAGGGG 1900
GAGGAATTCCAGTCTTCTCTCCAGA 1925
GCCCTGTGAGCATCTGCTCCTCCTC 1950
CACTCCATCCAGTCTTCCCCAGAGT 1975
TTCCCTGAGAGTTCTCAGAGTCCTC 2000
CTGAGGGGCCTGTCCAGTCTCCTCT 2025
CCATAGTCCTCAGAGCCCTCCTGAG 2050
GGGATGCACTCCCAATCTCCTCTCC 2075
AGAGTCCTGAGAGTGCTCCTGAGGG 2100

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Figure 1(D)

GGAGGATTCCTGTCTCCTCTCCAA 2125
 ATTCCTCAGAGTCCTCTTGAGGGAG 2150
 AGGACTCCCTGTCTTCTCTCCATTT 2175
 TCCTCAGAGTCCTCCTGAGTGGGAG 2200
 GACTCCCTCTCTCCTCTCCACTTTC 2225
 CTCAGTTTCCTCCTCAGGGGGAGGA 2250
 CTTCCAGTCTTCTCTCCAGAGTCCT 2275
 GTGAGTATCTGCTCCTCCTCCACTT 2300
 CTTTGAGTCTTCCCCAGAGTTTCCC 2325
 TGAGAGTCCTCAGAGTCCTCCTGAG 2350
 GGGCCTGCTCAGTCTCCTCTCCAGA 2375
 GACCTGTCAGCTCCTTCTTCTCCTA 2400
 CACTTTAGCGAGTCTTCTCCAAAGT 2425
 TCCCATGAGAGTCCTCAGAGTCCTC 2450
 CTGAGGGGCCTGCCCAGTCTCCTCT 2475
 CCAGAGTCCTGTGAGCTCCTTCCCC 2500
 TCCTCCACTTCATCGAGTCTTTCCC 2525
 AGAGTTCTCCTGTGAGCTCCTTCCC 2550
 CTCCTCCACTTCATCGAGTCTTTCC 2575
 AAGAGTTCCCCTGAGAGTCCTCTCC 2600
 AGAGTCCTGTGATCTCCTTCTCCTC 2625
 CTCCACTTCATTGAGCCCATTAGT 2650
 GAAGAGTCCAGCAGCCCAGTAGATG 2675

SL26

AATATACAAGTTCCTCAGACACCTT 2700
 GCTAGAGAGTGATTCCCTTGACAGAC 2725
 AGCGAGTCCTTGATAGAGAGCGAGC 2750
 CCTTGTTCACTTATACTGGATGA 2775
 AAAGGTGGACGAGTTGGCGCGGTTT 2800

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Figure 1(E)

CTTCTCCTCAAATATCAAGTGAAGC 2825
SL27
AGCCTATCACAAAGGCAGAGATGCT 2850
GACGAATGTCATCAGCAGGTACACG 2875
GGCTACTTTCCTGTGATCTTCAGGA 2900
AAGCCCGTGAGTTCATAGAGATACT 2925
TTTTGGCATTTCCTTGAGAGAAGTG 2950
GACCCTGATGACTCCTATGTCTTTG 2975
TAAACACATTAGACCTCACCTCTGA 3000
GGGGTGTCTGAGTGATGAGCAGGGC 3025
ATGTCCCAGAACCGCCTCCTGATTC 3050
TTATTCTGAGTATCATCTTCATAAA 3075
GGGCACCTATGCCTCTGAGGAGGTC 3100
ATCTGGGATGTGCTGAGTGGAATAG 3125
GGGTGCGTGCTGGGAGGGAGCACTT 3150
TGCCTTTGGGGAGCCCAGGGAGCTC 3175
CTCACTAAAGTTTGGGTGCAGGAAC 3200
ATTACCTAGAGTACCGGGAGGTGCC 3225
CAACTCTTCTCCTCCTCGTTACGAA 3250
TTCCTGTGGGGTCCAAGAGCTCATT 3275
CAGAAGTCATTAAGAGGAAAGTAGT 3300
AGAGTTTTTGGCCATGCTAAAGAAT 3325
ACCGTCCCTATTACCTTTCCATCCT 3350
CTTACAAGGATGCTTTGAAAGATGT 3375
GGAAGAGAGAGCCCAGGCCATAATT 3400
GACACCACAGATGATTCGACTGCCA 3425
CAGAAAGTGCAAGCTCCAGTGTCAT 3450
GTCCCCCAGCTTCTCTTCTGAGTGA 3475
AGTCTAGGGCAGATTCTTCCCTCTG 3500

10085108-030102

Figure 1(F)

AGTTTGAAGGGGGCAGTCGAGTTTC 3525
TACGTGGTGGAGGGCCTGGTTGAGG 3550
CTGGAGAGAACACAGTGCTATTTGC 3575
ATTTCTGTTCCATATGGGTAGTTAT 3600
GGGGTTTACCTGTTTTACTTTTGGG 3625
TATTTTTCAAATGCTTTTCCTATTA 3650
ATAACAGGTTTAAATAGCTTCAGAA 3675
TCCTAGTTTATGCACATGAGTCGCA 3700
CATGTATTGCTGTTTTTCTGGTTTA 3725
AGAGTAACAGTTTGATATTTTGTA 3750
AAACAAAAACACCCCAAACACACC 3775
ACATTGGGAAAACCTTCTGCCTCAT 3800
TTTGTGATGTGTCACAGGTTAATGT 3825
GGTGTTACTGTAGGAATTTTCTTGA 3850
AACTGTGAAGGAAGTCTGCAGTTAA 3875
ATAGTGGAATAAAGTAAAGGATTGT 3900
TAATGTTTGCATTTCCCTCAGGTCCT 3925
TTAGTCTGTTGTTCTTGAAAATAA 3950
AGATACATACCTGGTTTGCTTGGCT 3975
TACGTAAGAAAGTAGAAGAAAGTAA 4000
ACTGTAATAAATAAAAAAAAAAAAAA 4025
AAAAAA 4031

S A F P T T I N F T R Q R · Q P
TCGGCCTTCCCACTAGCAT CAACTTCACTCGACAGAGGC AACCC.....
.....galgaggaaggagg gaagcllccclccatlillc lcctclllccacillal

.76 .431

lccccgcgcctccctcgt ttttcttctcaccctcacc ctcctctcgcctcgcgtt cccaggggacacaggatatg cctactgctgggatgccgag 294
 intron III D K D M P T A G M P S 13
 exon IV

 TCCTCTCCAGAGTTCCTCTG AGAGTCCTCAGAGTTGTCTT GAGGGGGAGGACTCCAGTC TCCTCTCCAGATCCCCAGA GTTCTCTGAGAGCGACGAC 394
 L L Q S S S E S P Q S Y P E G E D S Q S P L O I P Q S S P E S D D 46

 ACCCTGTATCCTCTCCAGAG TCCTCAGAGTCGTTCTGAGG GGGAGGACTCCTCGGATCCT CTCCAGAGACCTCCTGAGGG GAAGGACTCCCAGTCTCCTC 494
 T L Y P L Q S P Q S R S E G E D S S D P L Q R P P E G K D S Q S P L 80

 TCCAGATTCCCCAGAGTTCT CCTGAGGGCGGACGACACCCA GTCCTCTCTCCAGATTCTC AGAGTTCTCTGAGGGGAAG GACTCCCTGCTCCTCTAGA 594
 Q I P Q S S P E G D D T Q S P L Q N S Q S S P E G K D S L S P L E 113

 GATTTCAGAGCCCTCCTG AGGTGAGGATGTCAGTCT CCTCTCAGAAATCCTGCGAG TTCCTTCTCTCCTCTGCTT TATTGAGTATTTCCAGAGT 694
 I S Q S P P E G E D V Q S P L Q N P A S S F F S S A L L S I F Q S 146

 TCCCCTGAGAGTATCAAG TCCTTTTGAGGGTTTTCCCC AGTCTGTTCTCCAGATTCTT GTGAGCGCGGCTCCTCCTC CACTTAGTGAGTATTTCC 794
 S P E S I Q S P F E G F P Q S V L Q I P V S A A S S S T L V S I F Q 180

 AGAGTCCCCTGAGAGTACT CAAAGTCCTTTTGAGGGTTT TCCCAGTCTCCACTCCAGA TTCCTGTGAGCGCGCTCCTTC TCCTCCACTTTATTGAGTAT 894
 S S P E S T Q S P F E G F P Q S P L Q I P V S R S F S S T L L S I 213

 TTTCCAGAGTCCCCTGAGA GAAGTCAGAGAACTCTGAG GGTTTGCACAGTCTCCCT CCAGATTCTCTGAGCTCCT CCTCGTCTCCACTTTACTG 994
 F Q S S P E R S Q R T S E G F A Q S P L Q I P V S S S S S S T L L 246

A1
C1 AGTCTTTCCAGAGTTCCCC TGAGAGAAGTCCAGTACTT TTGAGGGTTTTCCCCAGTCT CCACTCCAGATTCTGTGAG CCGCTCCTTCTCCTCCACTT 1094
S L F Q S S P E R T Q S T F E G F P Q S P L Q I P V S R S F S S T L 280

A1
C1 TATTGAGTATTTCCAGAGT TCCCTGAGAGAAGTCCAG TACTTTGAGGGTTTTGCC AGTCTCCTCTCCAGATTCTT GTGAGCTCCTCCTCCTCCTC 1194
L S I F O S S P E R T Q S T F E G F A Q S P L Q I P V S S S S S S 313

A1
C1 CACTTATTGAGTCTTTTCC AGAGTCCCTGAGAGAAGT CAGAGTACTTTTGAGGGTTT TCCCAGTCTCTCTCCAGATTCTTCCCTTCTC 1294
T L L S L F Q S S P E R T Q S T F E G F P Q S L L Q I P M T S S F 346

A1
C1 TCCTCTACTTTATTGAGTAT TTCCAGAGTCTCTCTGAGA GTGCTCAAAGTACTTTTGTAG GGTTCCTCCAGTCTCCTCT CCAGATTCTGGGAGCCCCCT 1394
S S T L L S I F Q S S P E S A Q S T F E G F P Q S P L Q I P G S P S 380

A1
C1 CCTCTCCTCCACTTACTG AGTCTTTCCAGAGTTCCCC TGAGAGAAGTCCAGTACTT TTGAGGGTTTTCCCCAGTCT CCTCTCCAGATTCTCTATGAC 1494
F S S T L L S L F Q S S P E R T H S T F E G F P Q S P L Q I P M T 413

A1
C1 CTCCTCCTTCTCCTCTACTT TATTGAGTATTTTACAGAGT TCTCCTGAGAGTGCTCAAAG TGCTTTTGAGGGTTTTCCCC AGTCTCCTCTCCAGATTCTCT 1594
S S F S S T L L S L L Q S S P E S A Q S A F E G F P Q S P L Q I P 446

A1
C1 GTGAGCTCCTCTCTCTCTA CACTTTATTGAGTCTTTTCC AGAGTCCCTGAGAGAAGT CAGAGTACTTTTGAGGGTTT TCCCAGTCTCTCTCTCCAGA 1694
V S S S F S Y T L L S L L F Q S S P E R T Q S T F E G F P Q S P L Q I 480

A1
C1 TTCTGTGAGCTCCTCTCCTC TCCCTCCAGTCTTTTGTAG TCTTTCCAGAGTCTCCCTG AGTGTACCAAGTACTTTT GAGGGTTTTCCCCAGTCTCC 1794
P V S S S S S T L L S L L F Q S S P E C T Q S T F E G F P Q S P 513

A1
C1 TCCTCAGATTCCTCAGAGTC CTCCTGAAGGGGAGATACC CATTCTCTCTCCAGATTGT TCCAAGTCTCTCAGTGGG AGGACTCCCTGTCCTCCTCAC 1894
L Q I P Q S P P E G E N T H S P L Q I V P S L P E W E D S L S P H 546

A1
C1 TACTTCTCCTCAGAGCCCTCC TCAGGGGAGGACTCCCTAT CTCTCCTCCTCTCTCCTCAG AGCCCTCCTCAGGGGAGGA CTCCTGTCTCCTCCTACTACT 1994
Y F P Q S P P Q G E D S L S P H Y F P Q S P Q G E D S L S P H Y F 580

A1
C1 TTCTCAGAGCCCTCAGGGG GAGGACTCCCTGTCCTCCTCA CTACTTCTCCTCAGAGCCCTC CTCAGGGGAGGACTCCATG TCTCCTCTCTACTTTCTCTCA 2094
P Q S P Q G E D S L S P H Y F P Q S P P Q G E D S M S P L Y F P Q 613

A1
C1 GAGTCTCTCAGGGGAGG AATCCAGTCTCTCTCTCCAG AGCCCTGTGAGCATCTGCTC CTCTCCTCCTCCTCCTCCTGAG 2194
S P L Q G E F Q S S L Q S P V S I C S S S T P S L P Q S F P E 646

A1
C1 AGTCTCAGAGTCTCTCCTCA GGGCCCTGTCCAGTCTCTC TCCATAGTCTCCTCAGAGCCCT CCTGAGGGGAGTCCCTCCCA ATCTCTCTCTCCTCCTGAG 2294
S S Q S P P E G P V Q S P L H S P Q S P P E G M H S Q S P L Q S P E 680

A1
C1 AGAGTCTCTCAGGGGAG GATTCCTGTCCTCTCTCCA AATTCCTCAGAGTCTCTG AGGGAGAGGACTCCCTGCTC TCCTCTCCTCTCCTCAGAG 2394
S A P E G E D S L S P L Q I P Q S P L E G E D S L S S L H F P Q S 713

A1
C1 TCCTCCTGAGTGGGAGGACT CCCCTCTCTCTCTCCTCTT CCTCAGTCTCTCTCCTCAGGG GGAGGACTTCCAGTCTCTC TCCAGAGTCTCTGAGTATC 2494
P P E W E D S L S P L H F P Q F P P Q G E D F Q S S L Q S P V S I 746

A1
C1 TGCTCTCTCTCCTCCTCTT GAGTCTCTCTCCTCAGAGTCTC CTGAGAGTCTCTCAGAGTCTCCT CCTGAGGGGCTCTGCTCAGTC TCCTCTCCTCAGAGAGCTGTCA 2594
C S S T S L S L P Q S F P E S P Q S P P E G P A Q S P L Q R P V S 780

A1
C1 GCTCTCTCTCTCTCTCCTT TAGCGAGTCTCTCTCCTCAAG TTCCCATGAGAGTCTCTCAGA GTCTCTCTCAGGGGCTGCTGCC CAGTCTCTCTCTCCTCAGAGTCC 2694
S F F S Y T L A S L L Q S S H E S P Q S P P E G P A Q S P L Q S P 813

A1

C1 TGAGACTCCTTCCCCCTCCT CCACCTTCATCGAGTCTTTCC CAGAGTTCTCCTGTGAGCTC CTTCCCTCCTCCACTTCAT CGAGTCTTTCCAAGAGTTCC 2794
[V_S_S_F_P_S_S_T_S_S_S_L_S_Q_S_S_P|V_S_S_F_P_S_S_T_S_S|S_L_S_K_S_S 846

41

	-----	S E G S S S R E E E G P S 89
CCTGAGAGTCCCTCCAGAG TCCTGTGATCTCCTTCCT CCTCCACTTCATTGAGCCCA TTACGTGAAGAGTCCAGCAG CCGTGAAGAGGAGGGGCCAA 468		
P E S P L Q S . P V I S F S S S T S L S P S S E E S S S P V D E Y T S 880		

[illegible][illegible]

2

P E I F G K A S E S L Q L V F G I D V K E A D P T G H S Y V L V T C 174
CCTGAGATCTTCGGCAAAGC CTCTGAGTCTTCGACGTGG TCTTTGGCAITGACGTGAAG GAAGCAGACCCACCGGCCA CTCCATATGCTCTTGTCACCT 723
CCTGTGATCTTCAGGAAAGC CCGTGAGTTCATAGAGATAC TTTTGGCAITTCCTGAGA GAAGTGGACCCCT...GATGA CTCCTATGCTCTTGTAACA 3191
P V I F R K A R E F I E I L F G I S L R E V D P . D D S Y V F V N T 979

L G L S Y D G L L G D N Q I M P K T G F L I I V L V M I A M E G 207
GCCTAGGTCCTCCTATGAT GGCCTGCTGGTGATAATCA GATCATGCCCAAGACAGGCT TCCTGATAATTGCTCTGGTC ATGATTGCAATGGAGGGCGG 823
CATTAGACCTCACCTCTGAG GGGTGCTGAGTGATGAGCA GGGCATGTCCCAGAACCGCC TCCTGATTCTTATTCIGAGT ATCATCTTCATAAAGGGCAC 3291
L D L T S E G C L S D E O G M S Q N R L L I L I L S I I F I K G T 1012

II A P E E I W E E L S F M E V Y D G R E H S A Y G E P R K L L T	240
CCATGCTCTGAGGAGGANA TCTGGGAGGAGCTGAGTGTG ATGGAGGCTGATGATGGGAG GGAGCACAGTGCCTATGGGG AGCCGAGGAAGCTGCTCACC	923
CTATGCCCTCTGAGGAGGTCA TCTGGGATGTGCTGAGTGGG AAGGGGTGCGTGGTGGGAG GGAGCACATTGCCCTTTGGGG AGCCGAGGAGCTCCTCACT	3391
Y A S E E V I W D V L S G I G Y R A G R E H F A F G E P R E L L T	1015

Q D L V Q E K Y L E Y R Q V P D S D P A R Y E F L W G P R A L A E T 274
 CAGATTGGTGAGGAAA GTACCTGGAGTACCGGAGG TGCCGGACAGTGATCCGCA CGCIATGAGTTCCTGIGGGG TCCAAGGGCCCTCGCTGAAA 1023
 AAGTTTGGGTGAGGAACA TTACCTAGAGTACCGGGAGG TGCCCAACTCTCTCTCCT CGTIACGAATTCCTGIGGGG TCCAAGAGCTCATTGAGAAG 3491
 < V W V Q E H Y L E Y R E V P N S S P P R Y E F L W G P R A H S E V 1079

S Y V K V L E Y V I K V S A R V R F F P S L R E A A L R E E E 307
 CCAGCTATGTGAAAGTCCTT GAGTATGTGATCAAGGTCAG TGCAAGAGTTCGCTTTTCT TCCATCCCTGCGTGAAGCA GCITTGAGAGAGGAGGAAGA 1123
 TCAITTAAGAGGAAAGTAGTA GAGTTTTGGCCATGCTAAA GAATACCGTCCCTATTACCT TTCCATCCTCTTACAAGGAT GCITTTGAAGATGTGGAAGA 3591
 I K R K V V E F L A M L K N T V P I T F P S S Y K D A L K D V E E 1112

G V OPA 309
 GGGAGTCGAGCATGAGTTG CAGCCAAGGCCAGTGGAGG GGGACTGGGCCAGTGCACCT TCCAGGGCCGCTCCAGCAG CTTCCTCCCTGCTGTGAC 1223
 GAGAGCCCGCCCATATTG ACACCACAGATGATTCGACT GCCACAGAAAGTGAAGCTC CAGTGTCTATGTCCTCCAGCT TCTCTTCTGAGTGAAGTCTA 3691
 R A Q A I I D T T D S T A T E S A S S V M S P S F S S E OPA 1142

---ATGAGGCCCATCTTCA CTCGAAGAGAGCGGTCAGT GTTCTCAGTAGTAG-----GTTTC 1279
 GGGCAGATCTTCCCTCTGA GTTGAAGGGGGCAGTCGAG TTTCTACGTGGTGGAGGGCC TGGTTGAGGCTGGAGAGAAC ACAGTGTCTATTGCAATTTCT 3791

TGTTCTATTGGGTGACTGG AGATTIACTTTGTTCTTT TTGGAATTGTCAAAATGTTT TT--TTTTAAGGGATGGTTG AATGAACITTCAGCATCCAAG 1377
 GTTCCATATGGGTAGTATG GGGTTTACCTGTTTACITTT TGGGTATTTTCAAAATGCTT TTCTATTATAACACAGGTTT AATAGCTTCAGAATCCTAG 3891

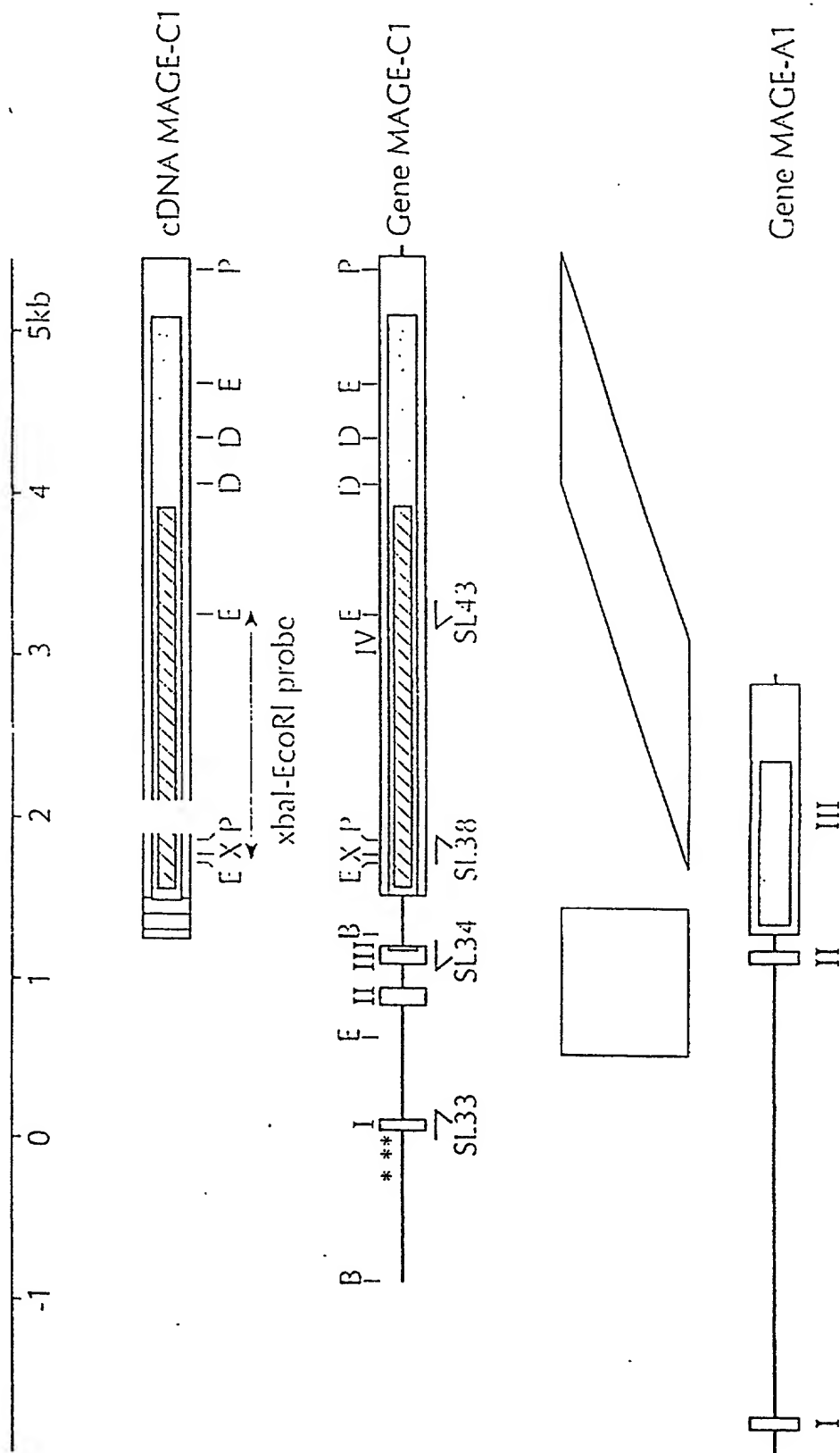
TTTATGAATGACAGCAGT-C ACACAGTTCTGTGTATATAG TTTAAGGGTAAGAGTCTTGT GTTTTATTCAGATTGGGAAA TCCATTCTATTTTGTGAATT 1476
 TTTATGCACATGAGTCGCAC ATGTATTGCTGTTTTCTGG TTTAAGAGTAAACAGTTTGAT ATTTTGTAACAAACAAAAACA CACCCAAACACACACCATG 3991

GGGATAATAACAGCAGTGGG ATAAGTACTTAGAATGTGA AAAATGAGCAGTAAATAGA TGAGATAAAGAACTAAAGAA ATTAAGAGATAGTCAATCT 1576
 GGAAACCTTCTGCCTCATT TTGTGATGTGTCACAGGITA ATGTGGTGTACGTAGGAA TTTTCTTGAACACTGTGAAGG AACCTGCGAGTTAAATAGTG 4091

TGCCTTATACCTCAGTCTAT TCTGTAAAATTTTTAAAGAT ATAIGCATACCTGGATTCC TTGGCTTCTTTGAGAATGTA AGAGAAATTAATCTGAATA 1676
 GAATAAGTAAGGATTGTT AATGTTTGCATTTCCTCAGG TCCCTTAGTCTGTGTTCTT GAAACTAAAGATACATACC TGGTTTGTCTGGCTTACGTA 4191

AAGAATCTTCTCTGT.....
 AGAAAGTAGAAGAAAGTAAA CTGTAATAATAAA 1691
 4225

FIG. 3



10
15
20
25
30

5

25

30

Figure 6 Amino-acid sequence of the putative MAGE-C3 protein (SEQ ID NO: 22)

	MPLFPNLPRLSFEEDFQNPSVTEDLVDAQDSIDEEEDASSTSSSSFHFL	50
5	FPSSSSLSSSSPLSSPLPSTLILGVPEDEDMPAAGMPPLPQSPPEIPPQG	100
	PPKISPQGPPQSPPQSPLDSCSSPLLWTRLDEESSSEEDTATWHPALPES	150
	ESLPRYALDEKVAELVQFLLLLKYQTKEPVTKAEMLTTVIKKYKDYFPMIF	200
	GKAHEFIELIFGIALTDMDPDNHSYFFEDTLDLTYEGSLIDDQGMPKNCL	250
	LILILSMIFIKGSCVP EEVIWEVLSAIGVCAGREHFIYGDPRKLLTIHWV	300
10	QRKYLEYREVPNSAPPRYEFLWGPRAHSEASKRSLRVFIQAIQYHP	346

1005100.030102
201000.001500

Figure 7 Nucleotide sequence of gene MAGE-B5
(SEQ ID NO: 23)

This sequence is the antiparallel sequence corresponding to nucleotides 123358 to 124185 of BAC clone 466O4 (GenBank accession number AC005297). The sequence has been renumbered in this figure, taking the first nucleotide of the start codon as nucleotide number 1.

Primers SL189 and SL190 that were used in the RT-PCR assay are indicated.

ATGACTTCTGCAGGTGTTTTTAATGCAGGATCTGACGAAAGGGCTAACAG 50
TAGAGATGAGGAGTACCCATGTTCTCAGAGGTCTCACCTCCACTGAGA 100
GTTTCATGCAGCAATTTCAATAATTAAGGTGGGTTTGTTGGAGCAGTTC 150
CTGCTCTACAAGTTCAAAATGAAACAGCGTATTTTGAAGGAAGATATGCT 200
GAAGATTGTCAACCCAAGATACCAAAACAGTTTGCTGAGATTACAGAA 250
GAGCTTCTGAGCACATTGAGGTGTCTTTGCACTTGACTTGAAGGAAGTC 300
AACCCAACCTGTCACTTATATGACCTTGTCAGCAAGCTGAAACTCCCCAA 350
CAATGGGAGGATTTCATGTTGGCAAAGTGTACCCAAGACTGGTCTCCTCA 400
SL189
TGACTTTCCTGGTTGTGATCTTCCTGAAAGGCAACTGTGCCAACAAGGAA 450
GATACCTGGAAATTTCTGGATATGATGCAAATATATGATGGGAAGAAGTA 500
CTACATCTATGGAGAGCCCAGGAAGCTCATCACTCAGGATTTCTGTGAGGC 550
TAACGTACCTGGAGTACCACCAGGTGCCCTGCAGTTATCCTGCACACTAT 600
CAATTCCTTTGGGGTCCAAGAGCCTATACTGAAACCAGCAAGATGAAAGT 650
CCTGGAATATTTGGCCAAGGTCAATGATATTGCTCCAGGTGCCTTCTCAT 700
SL190
CACAAATATGAAGAGGCTTTGCAAGATGAGGAAGAGAGCCCAAGCCAGAGA 750
TGCAGCCGAAACTGGCACTACTGCAGTGGCCAAGACTGTCTCAGGGCGAA 800
GTTTCAGCAGCTTCTCTCAACCCTATTGA 828

Figure 8 Amino-acid sequence of the putative MAGE-B5 protein (SEQ ID NO: 24)

	MTSAGVFNAGSDERANSRDEEYPCSSSEVSPSTESSCSNFINIKVGLLEQF	50
5	LLYKFKMKQRILKEDMLKIVNPRYQNQFAEIHRRASEHIEVVFAVDLKEV	100
	NPTCHLYDLVSKLKLNNNGRIHVGVLPKTGLLMTFLVVIFLKGNCANKE	150
	DTWKFLDMMQIYDGKKYIYGEPRKLITQDFVRLTYLEYHQVPCSYPAHY	200
	QFLWGPRAYTETSKMKVLEYLAKVNDIAPGAFSSQYEEALQDEEESPSQR	250
	CSRNWHYCSGQDCLRAKFSSFSQPY	275

10

1005100 030402
201002 801500T

Figure 9 Nucleotide sequence of gene MAGE-B6
(SEQ ID NO: 25)

This sequence is the antiparallel sequence corresponding to nucleotides 146417 to 147640 of BAC clone 466O4 (GenBank accession number AC005297). The sequence has been renumbered in this figure, taking the first nucleotide of the start codon as nucleotide number 1.

Primers SL191 and SL192 that were used in the RT-PCR assay are indicated.

10 ATGCCCTCGGGGTCACAAGAGTAAGCTCCGTACCTGTGAGAAACGCCAAGA 50
GACCAATGGTCAGCCACAGGGTCTCACGGGTCCCCAGGCCACTGCAGAGA 100
AGCAGGAAGAGTCCCACTCTTCTCATCTCTTCTCGCGCTGTCTGGGT 150
SL191
GATTGTCGTAGGTCTTCTGATGCCTCCATTCCTCAGGAGTCTCAGGGAGT 200
GTCACCCACTGGGTCTCCTGATGCAGTTGTTTCATATTCAAATCCGATG 250
TGGCTGCCAACGGCCAAGATGAGAAAAGTCCAAGCACCTCCCGTGATGCC 300
TCCGTTCCCTCAGGAGTCTCAGGGAGCTTACCCACTGGCTCTCCTGATGC 350
AGGTGTTTTAGGCTCAAATATGATGTGGCTGCCAACGGCCAAGATGAGA 400
AAAGTCCAAGCACTTCCCATGATGTCTCCGTTCTCAGGAGTCTCAGGGA 450
GCTTACCCACTGGCTCGCCTGATGCAGGTGTTTCAGGCTCAAATATGA 500
TGTGGCTGCCGAGGGTGAAGATGAGGAAAGTGTAAAGCGCTCACAGAAAG 550
SL192
CCATCATTTTTAAGCGCTTAAGCAAAGATGCTGTAAAGAAGAAGCGGTGC 600
ACGTTGGCGCAATTCTTCGAGAAGAAGTTTGAGAAGAAGAGTCCATTTT 650
25 GAAGGCAGACATGCTGAAGTGTGTCCGCAGAGAGTACAAGCCCTACTTCC 700
CTCAGATCCTCAACAGAACCTCCCAACATTTGGTGGTGGCCTTTGGCGTT 750
GAATTGAAAGAAATGGATTCCAGCGGCGAGTCTACACCCTTGTCAGCAA 800
GCTAGGCCTCCCCAGTGAAGGAATTCTGAGTGGTGATAATGCGCTGCCGA 850
AGTCGGGTCTCCTGATGTGCTCCTGGTTGTGATCTTCATGAACGGCAAC 900
30 TGTGCCACTGAAGAGGAGGTCTGGGAGTTCTGGGTCTGTTGGGGATATA 950
TGATGGGATCCTGCATTCAATCTATGGGGATGCTCGGAAGATCATTACTG 1000
AAGATTTGGTGCAAGATAAGTACGTGGTTTACGGGCAGGTGTGCAACAGT 1050
GATCCTCCATGCTATGAGTTCCTGTGGGGTCCACGAGCCTATGCTGAAAC 1100
CACCAAGATGAGAGTCTGCGTGTTTTGGCCGACAGCAGTAACACCAGTC 1150
35 CCGGTTTATACCCACATCTGTATGAAGACGCTTTGATAGATGAGGTAGAG 1200
AGAGCATTGAGACTGAGAGCTTAA 1224

Figure 10 Amino-acid sequence of the putative MAGE-B6 protein (SEQ ID NO: 26)

	MPRGHKSKLRTCEKRQETNGQPQGLTGPDQATAEKQEESHSSSSSSSRACLG	50
5	DCRRSSDASIPQESQGVSPDGVSYSKSDVAANGQDEKSPSTSRDA	100
	SVPQESQGASPTGSPDAGVSGSKYDVAANGQDEKSPSTSHDVSVQESQG	150
	ASPTGSPDAGVSGSKYDVAEEGEDEESVSASQKAIIFKRLSKDAVKKKAC	200
	TLAQFLQKKFEKKESILKADMLKCVREYKPYFPQILNRTSQHLVVAFGV	250
	ELKEMDSSGESYTLVSKLGLPSEGILSGDNALPKSGLLMSLLVVFMMGN	300
10	CATEEEVWEFLGLLGIYDGILHSIYGDARKIITEDLVQDKYVVYRQVCNS	350
	DPPCYEFLWGPRAYAETTKMRVLRVLADSSNTSPGLYPHLYEDALIDEVE	400
	RALRLRA	407

10035108.030403